

## SEQUENCE LISTING

<110> FUJIWARA, TSUTOMU  
WATANABE, TAKESHI  
HORIE, MASATO

<120> AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN  
SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME

<130> Q-53599

<140> 09/273,565

<141> 1999-03-22

<150> 09/055,699

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<151> 1996-03-19

<150> JP 69163/1997

<151> 1997-03-05

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<170> PatentIn Ver. 2.1

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35 40 45

Pro Gly Glu Arg Glu Leu Thr Ile Pro Ala Ser Ala Asn Val Phe Tyr  
50 55 60

Pro Met Asp Gly Ala Ser His Asp Phe Leu Leu Arg Gln Arg Arg Arg  
65 70 75 80

Ser Ser Thr Ala Thr Pro Gly Val Thr Ser Gly Pro Ser Ala Ser Gly  
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Tyr Lys Ser Ile Leu Val Thr Ser Gln Asp Lys Ala Pro Ser Val Ile  
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Ser Arg Val Leu Lys Lys Asn Asn Arg Asp Ser Ala Val Ala Ser Glu  
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Tyr Glu Leu Val Gln Leu Leu Pro Gly Glu Arg Glu Leu Thr Ile Pro  
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gcc tcg gct aat gta ttc tac ccc atg gat gga gct tca cac gat ttc 246  
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Leu Leu Arg Gln Arg Arg Arg Ser Ser Thr Ala Thr Pro Gly Val Thr  
75 80 85

agt ggc ccg tct gcc tca gga act cct ccg agt gag gga gga ggg ggc 342  
 Ser Gly Pro Ser Ala Ser Gly Thr Pro Pro Ser Glu Gly Gly Gly Gly  
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tcc ttt ccc agg atc aag gcc aca ggg agg aag att gca cgg gca ctg 390  
 Ser Phe Pro Arg Ile Lys Ala Thr Gly Arg Lys Ile Ala Arg Ala Leu  
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Asp Val Ser Arg Val Glu Lys Tyr Thr Ile Ser Gln Glu Ala Tyr Asp  
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Gln Arg Gln Asp Thr Val Arg Ser Phe Leu Lys Arg Ser Lys Leu Gly  
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Arg Tyr Asn Glu Glu Glu Arg Ala Gln Gln Glu Ala Glu Ala Ala Gln  
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Arg Leu Ala Glu Glu Lys Ala Gln Ala Ser Ser Ile Pro Val Gly Ser  
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Arg Cys Glu Val Arg Ala Ala Gly Gln Ser Pro Arg Arg Gly Thr Val  
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Met Tyr Val Gly Leu Thr Asp Phe Lys Pro Gly Tyr Trp Ile Gly Val  
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 Gly Ile Ser Glu Phe Ile Val Met Ala Ala Asp Ala Glu Pro Leu Glu  
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 Ile Ile Leu His Leu Pro Leu Leu Cys Glu Asp Lys Asn Val Pro Tyr  
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cca aag gcc tat ccc ctt gcc gat gcc cac ctc acc aag aag cta ctg 163  
 Pro Lys Ala Tyr Pro Leu Ala Asp Ala His Leu Thr Lys Lys Leu Leu  
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 Asp Leu Val Gln Gln Ser Cys Asn Tyr Lys Gln Leu Arg Lys Gly Ala  
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aat gag gcc acc aaa acc ctc aac agg ggc atc tct gag ttc atc gtg 259  
 Asn Glu Ala Thr Lys Thr Leu Asn Arg Gly Ile Ser Glu Phe Ile Val  
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atg gct gca gac gcc gag cca ctg gag atc att ctg cac ctg ccg ctg 307  
 Met Ala Ala Asp Ala Glu Pro Leu Glu Ile Ile Leu His Leu Pro Leu  
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 35 40 45

Arg Cys Leu Tyr Arg Asp Val Met Leu Glu Leu Tyr Ser His Leu Phe  
 50 55 60

Ala Val Gly Tyr His Ile Pro Asn Pro Glu Val Ile Phe Arg Met Leu  
 65 70 75 80

Lys Glu Lys Glu Pro Arg Val Glu Glu Ala Glu Val Ser His Gln Arg  
 85 90 95

Cys Gln Glu Arg Glu Phe Gly Leu Glu Ile Pro Gln Lys Glu Ile Ser  
 100 105 110

Lys Lys Ala Ser Phe Gln Lys Asp Met Val Gly Glu Phe Thr Arg Asp  
 115 120 125

Gly Ser Trp Cys Ser Ile Leu Glu Glu Leu Arg Leu Asp Ala Asp Arg  
 130 135 140

Thr Lys Lys Asp Glu Gln Asn Gln Ile Gln Pro Met Ser His Ser Ala  
 145 150 155 160

Phe Phe Asn Lys Lys Thr Leu Asn Thr Glu Ser Asn Cys Glu Tyr Lys  
 165 170 175



Asp Pro Gly Lys Met Ile Arg Thr Arg Pro His Leu Ala Ser Ser Gln  
 180 185 190  
 Lys Gln Pro Gln Lys Cys Cys Leu Phe Thr Glu Ser Leu Lys Leu Asn  
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 Leu Glu Val Asn Gly Gln Asn Glu Ser Asn Asp Thr Glu Gln Leu Asp  
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 Asp Val Val Gly Ser Gly Gln Leu Phe Ser His Ser Ser Ser Asp Ala  
 225 230 235 240  
 Cys Ser Lys Asn Ile His Thr Gly Glu Thr Phe Cys Lys Gly Asn Gln  
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 His Thr Gln Lys Lys Pro Asp Gly Cys Ser Glu Cys Gly Gly Ser Phe  
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 Asn Leu His Glu Cys Gly Lys Cys Gly Lys Ala Phe Met Pro Gln Leu  
 305 310 315 320  
 Lys Leu Ser Val Tyr Leu Thr Asp His Thr Gly Asp Ile Pro Cys Ile  
 325 330 335  
 Cys Lys Glu Cys Gly Lys Val Phe Ile Gln Arg Ser Glu Leu Leu Thr  
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 His Gln Lys Thr His Thr Arg Lys Lys Pro Tyr Lys Cys His Asp Cys  
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 Gly Lys Ala Phe Phe Gln Met Leu Ser Leu Phe Arg His Gln Arg Thr  
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 Arg Gln Tyr Ala Cys Ser Glu Cys Gly Lys Ala Phe Thr Gln Lys Ser  
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 Thr Leu Ser Leu His Gln Arg Ile His Ser Gly Gln Lys Ser Tyr Val  
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Gly Lys Ser Phe Ile Ser Lys Ser Gln Leu Asp Ile His His Arg Ile  
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 Ile Leu Ser Met His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Lys  
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 Cys Ser Glu Cys Gly Lys Ala Phe Thr Ser Lys Ser Gln Phe Lys Glu  
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 His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Val Cys Thr Glu Cys  
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 His Thr Arg Glu Arg Pro Phe Val Cys Tyr Lys Cys Gly Lys Ala Phe  
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 Lys Pro Tyr Glu Cys Leu Asp Cys Gly Lys Ser Phe Ser Lys Lys Pro  
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 Gln Leu Lys Val His Gln Arg Ile His Thr Gly Glu Arg Pro Tyr Val  
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Gly Ser Cys Glu Ala Ser Val Ser Phe Glu Asp Val Thr Val Asp Phe	
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Ser Arg Glu Glu Trp Gln Gln Leu Asp Pro Ala Gln Arg Cys Leu Tyr	
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Arg Asp Val Met Leu Glu Leu Tyr Ser His Leu Phe Ala Val Gly Tyr	
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His Ile Pro Asn Pro Glu Val Ile Phe Arg Met Leu Lys Glu Lys Glu	
70 75 80	
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Pro Arg Val Glu Glu Ala Glu Val Ser His Gln Arg Cys Gln Glu Arg	
85 90 95 100	

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105 110 115	
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Ser Ile Leu Glu Glu Leu Arg Leu Asp Ala Asp Arg Thr Lys Lys Asp	
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Glu Gln Asn Gln Ile Gln Pro Met Ser His Ser Ala Phe Phe Asn Lys	
150 155 160	
aaa aca ttg aac aca gaa agc aat tgt gaa tat aag gac cct ggg aaa	885
Lys Thr Leu Asn Thr Glu Ser Asn Cys Glu Tyr Lys Asp Pro Gly Lys	
165 170 175 180	
atg att cgc acg agg ccc cac ctt gct tct tca cag aaa caa cct cag	933
Met Ile Arg Thr Arg Pro His Leu Ala Ser Ser Gln Lys Gln Pro Gln	
185 190 195	
aaa tgt tgc tta ttt aca gaa agt ttg aag ctg aac cta gaa gtg aac	981
Lys Cys Cys Leu Phe Thr Glu Ser Leu Lys Leu Asn Leu Glu Val Asn	
200 205 210	
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Gly Gln Asn Glu Ser Asn Asp Thr Glu Gln Leu Asp Asp Val Val Gly	
215 220 225	
tct ggt cag cta ttc agc cat agc tct tct gat gcc tgc agc aag aat	1077
Ser Gly Gln Leu Phe Ser His Ser Ser Ser Asp Ala Cys Ser Lys Asn	
230 235 240	
att cat aca gga gag aca ttt tgc aaa ggt aac cag tgt aga aaa gtc	1125
Ile His Thr Gly Glu Thr Phe Cys Lys Gly Asn Gln Cys Arg Lys Val	
245 250 255 260	
tgt ggc cat aaa cag tca ctc aag caa cat caa att cat act cag aag	1173
Cys Gly His Lys Gln Ser Leu Lys Gln His Gln Ile His Thr Gln Lys	
265 270 275	
aaa cca gat gga tgt tct gaa tgt ggg ggg agc ttc acc cag aag tca	1221
Lys Pro Asp Gly Cys Ser Glu Cys Gly Gly Ser Phe Thr Gln Lys Ser	
280 285 290	
cac ctc ttt gcc caa cag aga att cat agt gta gga aac ctc cat gaa	1269
His Leu Phe Ala Gln Gln Arg Ile His Ser Val Gly Asn Leu His Glu	
295 300 305	
tgt ggc aaa tgt gga aaa gcc ttc atg cca caa cta aaa ctc agt gta	1317
Cys Gly Lys Cys Gly Lys Ala Phe Met Pro Gln Leu Lys Leu Ser Val	
310 315 320	

tat ctg aca gat cat aca ggt gat ata ccc tgt ata tgc aag gaa tgt	1365
Tyr Leu Thr Asp His Thr Gly Asp Ile Pro Cys Ile Cys Lys Glu Cys	
325 330 335 340	
ggg aag gtc ttt att cag aga tca gaa ttg ctt acg cac cag aaa aca	1413
Gly Lys Val Phe Ile Gln Arg Ser Glu Leu Leu Thr His Gln Lys Thr	
345 350 355	
cac act aga aag aag ccc tat aaa tgc cat gac tgt gga aaa gcc ttt	1461
His Thr Arg Lys Lys Pro Tyr Lys Cys His Asp Cys Gly Lys Ala Phe	
360 365 370	
ttc cag atg tta tct ctc ttc aga cat cag aga act cac agt aga gaa	1509
Phe Gln Met Leu Ser Leu Phe Arg His Gln Arg Thr His Ser Arg Glu	
375 380 385	
aaa ctc tat gaa tgc agt gaa tgt ggc aaa ggc ttc tcc caa aac tca	1557
Lys Leu Tyr Glu Cys Ser Glu Cys Gly Lys Gly Phe Ser Gln Asn Ser	
390 395 400	
acc ctc att ata cat cag aaa att cat act ggt gag aga cag tat gca	1605
Thr Leu Ile Ile His Gln Lys Ile His Thr Gly Glu Arg Gln Tyr Ala	
405 410 415 420	
tgc agt gaa tgt ggg aaa gcc ttt acc cag aag tca aca ctc agc ttg	1653
Cys Ser Glu Cys Gly Lys Ala Phe Thr Gln Lys Ser Thr Leu Ser Leu	
425 430 435	
cac cag aga atc cac tca ggg cag aag tcc tat gtg tgt atc gaa tgc	1701
His Gln Arg Ile His Ser Gly Gln Lys Ser Tyr Val Cys Ile Glu Cys	
440 445 450	
ggg cag gcc ttc atc cag aag gca cac ctg att gtc cat caa aga agc	1749
Gly Gln Ala Phe Ile Gln Lys Ala His Leu Ile Val His Gln Arg Ser	
455 460 465	
cac aca gga gaa aaa cct tat cag tgc cac aac tgt ggg aaa tcc ttc	1797
His Thr Gly Glu Lys Pro Tyr Gln Cys His Asn Cys Gly Lys Ser Phe	
470 475 480	
att tcc aag tca cag ctt gat ata cat cat cga att cat aca ggg gag	1845
Ile Ser Lys Ser Gln Leu Asp Ile His His Arg Ile His Thr Gly Glu	
485 490 495 500	
aaa cct tat gaa tgc agt gac tgt gga aaa acc ttc acc caa aag tca	1893
Lys Pro Tyr Glu Cys Ser Asp Cys Gly Lys Thr Phe Thr Gln Lys Ser	
505 510 515	
cac ctg aat ata cac cag aaa att cat act gga gaa aga cac cat gta	1941
His Leu Asn Ile His Gln Lys Ile His Thr Gly Glu Arg His His Val	
520 525 530	
tgc agt gaa tgc ggg aaa gcc ttc aac cag aag tca ata ctc agc atg	1989
Cys Ser Glu Cys Gly Lys Ala Phe Asn Gln Lys Ser Ile Leu Ser Met	
535 540 545	

cat cag aga att cac acc gga gag aag cct tac aaa tgc agt gaa tgt	2037
His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Ser Glu Cys	
550 555 560	
ggg aaa gcc ttc act tct aag tct caa ttc aaa gag cat cag cga att	2085
Gly Lys Ala Phe Thr Ser Lys Ser Gln Phe Lys Glu His Gln Arg Ile	
565 570 575 580	
cac acg ggt gag aaa ccc tat gtg tgc act gaa tgt ggg aag gcc ttc	2133
His Thr Gly Glu Lys Pro Tyr Val Cys Thr Glu Cys Gly Lys Ala Phe	
585 590 595	
aac ggc agg tca aat ttc cat aaa cat caa ata act cac act aga gag	2181
Asn Gly Arg Ser Asn Phe His Lys His Gln Ile Thr His Thr Arg Glu	
600 605 610	
agg cct ttt gtc tgt tac aaa tgt ggg aag gct ttt gtc cag aaa tca	2229
Arg Pro Phe Val Cys Tyr Lys Cys Gly Lys Ala Phe Val Gln Lys Ser	
615 620 625	
gag ttg att acc cat caa aga act cac atg gga gag aaa ccc tat gaa	2277
Glu Leu Ile Thr His Gln Arg Thr His Met Gly Glu Lys Pro Tyr Glu	
630 635 640	
tgc ctt gac tgt ggg aaa tcg ttc agt aag aaa cca caa ctc aag gtg	2325
Cys Leu Asp Cys Gly Lys Ser Phe Ser Lys Lys Pro Gln Leu Lys Val	
645 650 655 660	
cat cag cga att cac acg gga gaa aga cct tat gtg tgt tct gaa tgt	2373
His Gln Arg Ile His Thr Gly Glu Arg Pro Tyr Val Cys Ser Glu Cys	
665 670 675	
gga aag gcc ttc aac aac agg tca aac ttc aat aaa cac caa aca act	2421
Gly Lys Ala Phe Asn Asn Arg Ser Asn Phe Asn Lys His Gln Thr Thr	
680 685 690	
cat acc aga gac aaa tct tac aaa tgc agt tat tct gtg aaa ggc ttt	2469
His Thr Arg Asp Lys Ser Tyr Lys Cys Ser Tyr Ser Val Lys Gly Phe	
695 700 705	
acc aag caa tgaattccta gtgcatcagc atattcataa atgaaatata	2518
Thr Lys Gln	
710	
ctccgagttt cttgaagaag agaacatctt ctcagaatca ggtctaatta tatgttattg	2578
aattcatgct tcagaaaaac tctagggatg cactgcatgt gtgaacacat gataaaaaag	2638
tcattgcttta ttttagtgag ggcaattaca gagaaaagag taagcagaaa tgtccttctg	2698
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tataagcata tatataatat ataagcatat tattatatac aggttgagta tcccttctcc 2998  
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<210> 13

<211> 389

<212> PRT

<213> Homo sapiens

<400> 13

Met Ala Asp Pro Arg Asp Lys Ala Leu Gln Asp Tyr Arg Lys Lys Leu  
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Leu Glu His Lys Glu Ile Asp Gly Arg Leu Lys Glu Leu Arg Glu Gln  
 20 25 30

Leu Lys Glu Leu Thr Lys Gln Tyr Glu Lys Ser Glu Asn Asp Leu Lys  
 35 40 45

Ala Leu Gln Ser Val Gly Gln Ile Val Gly Glu Val Leu Lys Gln Leu  
 50 55 60

Thr Glu Glu Lys Phe Ile Val Lys Ala Thr Asn Gly Pro Arg Tyr Val  
 65 70 75 80

Val Gly Cys Arg Arg Gln Leu Asp Lys Ser Lys Leu Lys Pro Gly Thr  
 85 90 95

Arg Val Ala Leu Asp Met Thr Thr Leu Thr Ile Met Arg Tyr Leu Pro  
 100 105 110

Arg Glu Val Asp Pro Leu Val Tyr Asn Met Ser His Glu Asp Pro Gly  
 115 120 125



Asn Val Ser Tyr Ser Glu Ile Gly Gly Leu Ser Glu Gln Ile Arg Glu  
 130 135 140  
 Leu Arg Glu Val Ile Glu Leu Pro Leu Thr Asn Pro Glu Leu Phe Gln  
 145 150 155 160  
 Arg Val Gly Ile Ile Pro Pro Lys Gly Cys Leu Leu Tyr Gly Pro Pro  
 165 170 175  
 Gly Thr Gly Lys Thr Leu Leu Ala Arg Ala Val Ala Ser Gln Leu Asp  
 180 185 190  
 Cys Asn Phe Leu Lys Val Val Ser Ser Ser Ile Val Asp Lys Tyr Ile  
 195 200 205  
 Gly Glu Ser Ala Arg Leu Ile Arg Glu Met Phe Asn Tyr Ala Arg Asp  
 210 215 220  
 His Gln Pro Cys Ile Ile Phe Met Asp Glu Ile Asp Ala Ile Gly Gly  
 225 230 235 240  
 Arg Arg Phe Ser Glu Gly Thr Ser Ala Asp Arg Glu Ile Gln Arg Thr  
 245 250 255  
 Leu Met Glu Leu Leu Asn Gln Met Asp Gly Phe Asp Thr Leu His Arg  
 260 265 270  
 Val Lys Met Thr Met Ala Thr Asn Arg Pro Asp Thr Leu Asp Pro Ala  
 275 280 285  
 Leu Leu Arg Pro Gly Arg Leu Asp Arg Lys Ile His Ile Asp Leu Pro  
 290 295 300  
 Asn Glu Gln Ala Arg Leu Asp Ile Leu Lys Ile His Ala Gly Pro Ile  
 305 310 315 320  
 Thr Lys His Gly Glu Ile Asp Tyr Glu Ala Ile Val Lys Leu Ser Asp  
 325 330 335  
 Gly Phe Asn Gly Ala Asp Leu Arg Asn Val Cys Thr Glu Ala Gly Met  
 340 345 350  
 Phe Ala Ile Arg Ala Asp His Asp Phe Val Val Gln Glu Asp Phe Met  
 355 360 365  
 Lys Ala Val Arg Lys Val Ala Asp Ser Lys Lys Leu Glu Ser Lys Leu  
 370 375 380  
 Asp Tyr Lys Pro Val  
 385

&lt;210&gt; 14

&lt;211&gt; 1167

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 14

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gagatcgacg gccgtcttaa ggagttaagg gaacaattaa aagaacttac caagcagtat 120
gaaaagtctg aaaatgatct gaaggcccta cagagtgttg ggcagatcgt ggggtgaagtg 180
cttaaacagt taactgaaga aaaattcatt gttaaagcta ccaatggacc aagatatgtt 240
gtgggttgtc gtgcacagct tgacaaaagt aagctgaagc caggaacaag agttgctttg 300
gatatgacta cactaactat catgagatat ttgccgagag aggtggatcc actggtttat 360
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cagatccggg aattaagaga ggtgatagaa ttacctctta caaaccaga gttatttcag 480
cgtgtaggaa taatacctcc aaaaggctgt ttgttatatg gaccaccagg tacgggaaaa 540
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attgatttgc caaatgaaca agcaagatta gacatactga aaatccatgc aggtccatt 960
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gcagatctga gaaatgtttg tactgaagca ggtatgttcg caattcgtgc tgatcatgat 1080
ttttagtagc aggaagactt catgaaagca gtcagaaaag tggctgattc taagaagctg 1140
gagtctaaat tggactacaa acctgtg                                     1167

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&lt;210&gt; 15

&lt;211&gt; 1566

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (17)..(1183)

&lt;400&gt; 15

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gagacggctt ctcac atg gcg gac cct aga gat aag gcg ctt cag gac tac 52
Met Ala Asp Pro Arg Asp Lys Ala Leu Gln Asp Tyr
      1                      5                      10

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cgc aag aag ttg ctt gaa cac aag gag atc gac ggc cgt ctt aag gag	100
Arg Lys Lys Leu Leu Glu His Lys Glu Ile Asp Gly Arg Leu Lys Glu	
15 20 25	
tta agg gaa caa tta aaa gaa ctt acc aag cag tat gaa aag tct gaa	148
Leu Arg Glu Gln Leu Lys Glu Leu Thr Lys Gln Tyr Glu Lys Ser Glu	
30 35 40	
aat gat ctg aag gcc cta cag agt gtt ggg cag atc gtg ggt gaa gtg	196
Asn Asp Leu Lys Ala Leu Gln Ser Val Gly Gln Ile Val Gly Glu Val	
45 50 55 60	
ctt aaa cag tta act gaa gaa aaa ttc att gtt aaa gct acc aat gga	244
Leu Lys Gln Leu Thr Glu Glu Lys Phe Ile Val Lys Ala Thr Asn Gly	
65 70 75	
cca aga tat gtt gtg ggt tgt cgt cga cag ctt gac aaa agt aag ctg	292
Pro Arg Tyr Val Val Gly Cys Arg Arg Gln Leu Asp Lys Ser Lys Leu	
80 85 90	
aag cca gga aca aga gtt gct ttg gat atg act aca cta act atc atg	340
Lys Pro Gly Thr Arg Val Ala Leu Asp Met Thr Thr Leu Thr Ile Met	
95 100 105	
aga tat ttg ccg aga gag gtg gat cca ctg gtt tat aac atg tct cat	388
Arg Tyr Leu Pro Arg Glu Val Asp Pro Leu Val Tyr Asn Met Ser His	
110 115 120	
gag gac cct ggg aat gtt tct tat tct gag att gga ggg cta tca gaa	436
Glu Asp Pro Gly Asn Val Ser Tyr Ser Glu Ile Gly Gly Leu Ser Glu	
125 130 135 140	
cag atc cgg gaa tta aga gag gtg ata gaa tta cct ctt aca aac cca	484
Gln Ile Arg Glu Leu Arg Glu Val Ile Glu Leu Pro Leu Thr Asn Pro	
145 150 155	
gag tta ttt cag cgt gta gga ata ata cct cca aaa ggc tgt ttg tta	532
Glu Leu Phe Gln Arg Val Gly Ile Ile Pro Pro Lys Gly Cys Leu Leu	
160 165 170	
tat gga cca cca ggt acg gga aaa aca ctc ttg gca cga gcc gtt gct	580
Tyr Gly Pro Pro Gly Thr Gly Lys Thr Leu Leu Ala Arg Ala Val Ala	
175 180 185	
agc cag ctg gac tgc aat ttc tta aag gtt gta tct agt tct att gta	628
Ser Gln Leu Asp Cys Asn Phe Leu Lys Val Val Ser Ser Ser Ile Val	
190 195 200	
gac aag tac att ggt gaa agt gct cgt ttg atc aga gaa atg ttt aat	676
Asp Lys Tyr Ile Gly Glu Ser Ala Arg Leu Ile Arg Glu Met Phe Asn	
205 210 215 220	
tat gct aga gat cat caa cca tgc atc att ttt atg gat gaa ata gat	724
Tyr Ala Arg Asp His Gln Pro Cys Ile Ile Phe Met Asp Glu Ile Asp	
225 230 235	

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gct att ggt ggt cgt cgg ttt tct gag ggt act tca gct gac aga gag 772
Ala Ile Gly Gly Arg Arg Phe Ser Glu Gly Thr Ser Ala Asp Arg Glu
      240                      245                      250

att cag aga acg tta atg gag tta ctg aat caa atg gat gga ttt gat 820
Ile Gln Arg Thr Leu Met Glu Leu Leu Asn Gln Met Asp Gly Phe Asp
      255                      260                      265

act ctg cat aga gtt aaa atg acc atg gct aca aac aga cca gat aca 868
Thr Leu His Arg Val Lys Met Thr Met Ala Thr Asn Arg Pro Asp Thr
      270                      275                      280

ctg gat cct gct ttg ctg cgt cca gga aga tta gat aga aaa ata cat 916
Leu Asp Pro Ala Leu Leu Arg Pro Gly Arg Leu Asp Arg Lys Ile His
      285                      290                      295                      300

att gat ttg cca aat gaa caa gca aga tta gac ata ctg aaa atc cat 964
Ile Asp Leu Pro Asn Glu Gln Ala Arg Leu Asp Ile Leu Lys Ile His
      305                      310                      315

gca ggt ccc att aca aag cat ggt gaa ata gat tat gaa gca att gtg 1012
Ala Gly Pro Ile Thr Lys His Gly Glu Ile Asp Tyr Glu Ala Ile Val
      320                      325                      330

aag ctt tcg gat ggc ttt aat gga gca gat ctg aga aat gtt tgt act 1060
Lys Leu Ser Asp Gly Phe Asn Gly Ala Asp Leu Arg Asn Val Cys Thr
      335                      340                      345

gaa gca ggt atg ttc gca att cgt gct gat cat gat ttt gta gta cag 1108
Glu Ala Gly Met Phe Ala Ile Arg Ala Asp His Asp Phe Val Val Gln
      350                      355                      360

gaa gac ttc atg aaa gca gtc aga aaa gtg gct gat tct aag aag ctg 1156
Glu Asp Phe Met Lys Ala Val Arg Lys Val Ala Asp Ser Lys Lys Leu
      365                      370                      375                      380

gag tct aaa ttg gac tac aaa cct gtg taatttactg taagattttt 1203
Glu Ser Lys Leu Asp Tyr Lys Pro Val
      385

gatggctgca tgacagatgt tggcttattg taaaaataaa gttaaagaaa ataatgtatg 1263

tattggcaat gatgtcatta aaagtatatg aataaaaaata tgagtaacat cataaaaaatt 1323

agtaattcaa cttttaagat acagaagaaa tttgtatggt tgtaaagtt gcattttattg 1383

cagcaagtta caaagggaaa gtggtgaagc ttttcatatt tgctgcgtga gcatttttgta 1443

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aaa 1566

<210> 16
<211> 223
<212> PRT

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&lt;213&gt; Homo sapiens

&lt;400&gt; 16

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Val Val Thr Val Ser Asp Val Gln Glu Leu Met Arg Arg Lys Glu Glu
      20              25              30

Ile Glu Ala Gln Ile Lys Ala Asn Tyr Asp Val Leu Glu Ser Gln Lys
      35              40              45

Gly Ile Gly Met Asn Glu Pro Leu Val Asp Cys Glu Gly Tyr Pro Arg
 50              55              60

Ser Asp Val Asp Leu Tyr Gln Val Arg Thr Ala Arg His Asn Ile Ile
 65              70              75              80

Cys Leu Gln Asn Asp His Lys Ala Val Met Lys Gln Val Glu Glu Ala
      85              90              95

Leu His Gln Leu His Ala Arg Asp Lys Glu Lys Gln Ala Arg Asp Met
      100             105             110

Ala Glu Ala His Lys Glu Ala Met Ser Arg Lys Leu Gly Gln Ser Glu
      115             120             125

Ser Gln Gly Pro Pro Arg Ala Phe Ala Lys Val Asn Ser Ile Ser Pro
      130             135             140

Gly Ser Pro Ala Ser Ile Ala Gly Leu Gln Val Asp Asp Glu Ile Val
      145             150             155             160

Glu Phe Gly Ser Val Asn Thr Gln Asn Phe Gln Ser Leu His Asn Ile
      165             170             175

Gly Ser Val Val Gln His Ser Glu Gly Lys Pro Leu Asn Val Thr Val
      180             185             190

Ile Arg Arg Gly Glu Lys His Gln Leu Arg Leu Val Pro Thr Arg Trp
      195             200             205

Ala Gly Lys Gly Leu Leu Gly Cys Asn Ile Ile Pro Leu Gln Arg
      210             215             220

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&lt;210&gt; 17

&lt;211&gt; 669

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 17

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agcgactgcc aggagctgat gcggcgcaag gaggagatag aagcgcatat caaggccaac 120
tatgacgtgc tggaagcca aaaaggcatt gggatgaacg agccgctggt ggactgtgag 180

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gggtaccccc ggtcagacgt ggacctgtac caagtccgca ccgccaggca caacatcata 240  
 tgcttcgaga atgatcaciaa ggcagtgtat aagcaggtgg aggagggcct gcaccagctg 300  
 cacgctcgcg acaaggagaa gcaggccccg gacatggctg agggccacaa agaggccatg 360  
 agccgcaaac tgggtcagag tgagagccag ggccctccac gggccttcgc caaagtgaac 420  
 agcatcagcc ccggctcccc agccagcatc gcgggtctgc aagtggatga tgagattgtg 480  
 gagttcggct ctgtgaacac ccagaacttc cagtcactgc ataacattgg cagtgtgggtg 540  
 cagcacagtg aggggaagcc cctgaatgtg acagtgatcc gcagggggga aaaacaccag 600  
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 ctgcaaaga 669

<210> 18  
 <211> 1128  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (125)..(793)

<400> 18  
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 cacg atg tcc gac gag gaa gcg agg cag agc gga ggc tcc tcg cag gcc 169  
 Met Ser Asp Glu Glu Ala Arg Gln Ser Gly Gly Ser Ser Gln Ala  
 1 5 10 15  
 ggc gtc gtg act gtc agc gac gtc cag gag ctg atg cgg cgc aag gag 217  
 Gly Val Val Thr Val Ser Asp Val Gln Glu Leu Met Arg Arg Lys Glu  
 20 25 30  
 gag ata gaa gcg cag atc aag gcc aac tat gac gtg ctg gaa agc caa 265  
 Glu Ile Glu Ala Gln Ile Lys Ala Asn Tyr Asp Val Leu Glu Ser Gln  
 35 40 45  
 aaa ggc att ggg atg aac gag ccg ctg gtg gac tgt gag ggc tac ccc 313  
 Lys Gly Ile Gly Met Asn Glu Pro Leu Val Asp Cys Glu Gly Tyr Pro  
 50 55 60  
 cgg tca gac gtg gac ctg tac caa gtc cgc acc gcc agg cac aac atc 361  
 Arg Ser Asp Val Asp Leu Tyr Gln Val Arg Thr Ala Arg His Asn Ile  
 65 70 75  
 ata tgc ctg cag aat gat cac aag gca gtg atg aag cag gtg gag gag 409  
 Ile Cys Leu Gln Asn Asp His Lys Ala Val Met Lys Gln Val Glu Glu  
 80 85 90 95

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gcc ctg cac cag ctg cac gct cgc gac aag gag aag cag gcc cgg gac 457
Ala Leu His Gln Leu His Ala Arg Asp Lys Glu Lys Gln Ala Arg Asp
                100                105                110

atg gct gag gcc cac aaa gag gcc atg agc cgc aaa ctg ggt cag agt 505
Met Ala Glu Ala His Lys Glu Ala Met Ser Arg Lys Leu Gly Gln Ser
                115                120                125

gag agc cag ggc cct cca cgg gcc ttc gcc aaa gtg aac agc atc agc 553
Glu Ser Gln Gly Pro Pro Arg Ala Phe Ala Lys Val Asn Ser Ile Ser
                130                135                140

ccc ggc tcc cca gcc agc atc gcg ggt ctg caa gtg gat gat gag att 601
Pro Gly Ser Pro Ala Ser Ile Ala Gly Leu Gln Val Asp Asp Glu Ile
                145                150                155

gtg gag ttc ggc tct gtg aac acc cag aac ttc cag tca ctg cat aac 649
Val Glu Phe Gly Ser Val Asn Thr Gln Asn Phe Gln Ser Leu His Asn
                160                165                170                175

att ggc agt gtg gtg cag cac agt gag ggg aag ccc ctg aat gtg aca 697
Ile Gly Ser Val Val Gln His Ser Glu Gly Lys Pro Leu Asn Val Thr
                180                185                190

gtg atc cgc agg ggg gaa aaa cac cag ctt aga ctt gtt cca aca cgc 745
Val Ile Arg Arg Gly Glu Lys His Gln Leu Arg Leu Val Pro Thr Arg
                195                200                205

tgg gca gga aaa gga ctg ctg ggc tgc aac att att cct ctg caa aga 793
Trp Ala Gly Lys Gly Leu Leu Gly Cys Asn Ile Ile Pro Leu Gln Arg
                210                215                220

tgattgtccc tggggaacag taacaggaaa gcatcttccc ttgccctgga cttgggtcta 853

gggatttcca acttgtcttc tctccctgaa gcataaggat ctggaagagg cttgtaacct 913

gaacttctgt gtggtggcag tactgtggcc caccagtgtg atctccctgg attaaggcat 973

tcttaaaaac ttaggcttgg cctctttcac aaattaggcc acggccctaa ataggaattc 1033

cctggattgt gggcaagtgg gcggaagtta ttctggcagg tactggtgtg attattatta 1093

ttatttttaa taaagagttt tacagtgtg atatg 1128

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<210> 19
<211> 506
<212> PRT
<213> Homo sapiens

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<400> 19
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      20              25              30

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 35 40 45  
 Ser Ser Thr Ser Gly Ser Ser Ser Gly Ser Gly Ser Ser Ser Ser Ser  
 50 55 60  
 Ser Gly Ser Thr Ser Ser Arg Ser Arg Leu Tyr Arg Lys Lys Arg Val  
 65 70 75 80  
 Pro Glu Pro Ser Arg Arg Ala Arg Arg Ala Pro Leu Gly Thr Asn Phe  
 85 90 95  
 Val Asp Arg Leu Pro Gln Ala Val Arg Asn Arg Val Gln Ala Leu Arg  
 100 105 110  
 Asn Ile Gln Asp Glu Cys Asp Lys Val Asp Thr Leu Phe Leu Lys Ala  
 115 120 125  
 Ile His Asp Leu Glu Arg Lys Tyr Ala Glu Leu Asn Lys Pro Leu Tyr  
 130 135 140  
 Asp Arg Arg Phe Gln Ile Ile Asn Ala Glu Tyr Glu Pro Thr Glu Glu  
 145 150 155 160  
 Glu Cys Glu Trp Asn Ser Glu Asp Glu Glu Phe Ser Ser Asp Glu Glu  
 165 170 175  
 Val Gln Asp Asn Thr Pro Ser Glu Met Pro Pro Leu Glu Gly Glu Glu  
 180 185 190  
 Glu Glu Asn Pro Lys Glu Asn Pro Glu Val Lys Ala Glu Glu Lys Glu  
 195 200 205  
 Val Pro Lys Glu Ile Pro Glu Val Lys Asp Glu Glu Lys Glu Val Ala  
 210 215 220  
 Lys Glu Ile Pro Glu Val Lys Ala Glu Glu Lys Ala Asp Ser Lys Asp  
 225 230 235 240  
 Cys Met Glu Ala Thr Pro Glu Val Lys Glu Asp Pro Lys Glu Val Pro  
 245 250 255  
 Gln Val Lys Ala Asp Asp Lys Glu Gln Pro Lys Ala Thr Glu Ala Lys  
 260 265 270  
 Ala Arg Ala Ala Val Arg Glu Thr His Lys Arg Val Pro Glu Glu Arg  
 275 280 285  
 Leu Arg Asp Ser Val Asp Leu Lys Arg Ala Arg Lys Gly Lys Pro Lys  
 290 295 300  
 Arg Glu Asp Pro Lys Gly Ile Pro Asp Tyr Trp Leu Ile Val Leu Lys  
 305 310 315 320  
 Asn Val Asp Lys Leu Gly Pro Met Ile Gln Lys Tyr Asp Glu Pro Ile  
 325 330 335



Leu Lys Phe Leu Ser Asp Val Ser Leu Lys Phe Ser Lys Pro Gly Gln  
 340 345 350

Pro Val Ser Tyr Thr Phe Glu Phe His Phe Leu Pro Asn Pro Tyr Phe  
 355 360 365

Arg Asn Glu Val Leu Val Lys Thr Tyr Ile Ile Lys Ala Lys Pro Asp  
 370 375 380

His Asn Asp Pro Phe Phe Ser Trp Gly Trp Glu Ile Glu Asp Cys Lys  
 385 390 395 400

Gly Cys Lys Ile Asp Arg Arg Arg Gly Lys Asp Val Thr Val Thr Thr  
 405 410 415

Thr Gln Ser Arg Thr Thr Ala Thr Gly Glu Ile Glu Ile Gln Pro Arg  
 420 425 430

Val Val Pro Asn Ala Ser Phe Phe Asn Phe Phe Ser Pro Pro Glu Ile  
 435 440 445

Pro Met Ile Gly Lys Leu Glu Pro Arg Glu Asp Ala Ile Leu Asp Glu  
 450 455 460

Asp Phe Glu Ile Gly Gln Ile Leu His Asp Asn Val Ile Leu Lys Ser  
 465 470 475 480

Ile Tyr Tyr Tyr Thr Gly Glu Val Asn Gly Thr Tyr Tyr Gln Phe Gly  
 485 490 495

Lys His Tyr Gly Asn Lys Lys Tyr Arg Lys  
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<210> 20

<211> 1518

<212> DNA

<213> Homo sapiens

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 agcactagtg acagcagcag cagcagcagc actagtggca gcagcagcgg cagcggcagc 180  
 agcagcagca gcagcggcag cactagcagc cgcagccgct tgtatagaaa gaagagggtta 240  
 cctgagcctt ccagaagggc gcggcgggccc ccgttgggaa caaatttcgt ggataggctg 300  
 cctcaggcag ttagaaatcg tgtgcaagcg cttagaaaca ttcaagatga atgtgacaag 360  
 gtagataccc tgttcttaaa agcaattcat gatcttgaaa gaaaatatgc tgaactcaac 420  
 aagcctctgt atgataggcg gtttcaaata atcaatgcag aatacagagcc tacagaagaa 480  
 gaatgtgaat ggaattcaga ggatgaggag ttcagcagtg atgaggaggt gcaggataac 540

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accctagtg aaatgcctcc cttagagggg gaggaagaag aaaaccctaa agaaaaccca 600
gaggtgaaag ctgaagagaa ggaagttcct aaagaaattc ctgaggtgaa ggatgaagaa 660
aaggaagttg ctaaagaaat tcttgaggta aaggctgaag aaaaagcaga ttctaaagac 720
tgtatggagg caaccctga agtaaaagaa gatcctaaag aagtcccca ggtaaaggca 780
gatgataaag aacagcctaa agcaacagag gctaaggcaa gggctgcagt aagagagact 840
cataaaagag ttctgagga aaggcttcgg gacagtgtag atcttaaaag agctaggaag 900
ggaaagccta aaagagaaga ccctaaaggc attcctgact attggctgat tgttttaaag 960
aatgttgaca agctcgggcc tatgattcag aagtatgatg agccattct gaagttcttg 1020
tcggatgtta gcctgaagtt ctcaaacct ggccagcctg taagttacac ctttgaattt 1080
cattttctac ccaaccata cttcagaaat gaggtgctgg tgaagacata tataataaag 1140
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1518

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<210> 21
<211> 2636
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (266)..(1783)

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ccagctccgc tctgcgcgc tgctgccatc gccgctgcca cctccgcagc ccgggcctcc 180
gccgccgcca cccaagcatc cgtgagtcac tttctgcca tctctggctg cgcggtctcc 240
ctggtagagt ttgtaggctt gcaag atg gca gaa gca gat ttt aaa atg gtc 292
Met Ala Glu Ala Asp Phe Lys Met Val

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tcg gaa cct gtc gcc cat ggg gtt gcc gaa gag gag atg gct agc tcg	340
Ser Glu Pro Val Ala His Gly Val Ala Glu Glu Glu Met Ala Ser Ser	
10 15 20 25	
act agt gat tct ggg gaa gaa tct gac agc agt agc tct agc agc agc	388
Thr Ser Asp Ser Gly Glu Glu Ser Asp Ser Ser Ser Ser Ser Ser	
30 35 40	
act agt gac agc agc agc agc agc agc act agt ggc agc agc agc ggc	436
Thr Ser Asp Ser Ser Ser Ser Ser Ser Thr Ser Gly Ser Ser Ser Gly	
45 50 55	
agc ggc agc agc agc agc agc agc ggc agc act agc agc cgc agc cgc	484
Ser Gly Ser Ser Ser Ser Ser Ser Ser Gly Ser Thr Ser Ser Arg Ser Arg	
60 65 70	
ttg tat aga aag aag agg gta cct gag cct tcc aga agg gcg cgg cgg	532
Leu Tyr Arg Lys Lys Arg Val Pro Glu Pro Ser Arg Arg Ala Arg Arg	
75 80 85	
gcc ccg ttg gga aca aat ttc gtg gat agg ctg cct cag gca gtt aga	580
Ala Pro Leu Gly Thr Asn Phe Val Asp Arg Leu Pro Gln Ala Val Arg	
90 95 100 105	
aat cgt gtg caa gcg ctt aga aac att caa gat gaa tgt gac aag gta	628
Asn Arg Val Gln Ala Leu Arg Asn Ile Gln Asp Glu Cys Asp Lys Val	
110 115 120	
gat acc ctg ttc tta aaa gca att cat gat ctt gaa aga aaa tat gct	676
Asp Thr Leu Phe Leu Lys Ala Ile His Asp Leu Glu Arg Lys Tyr Ala	
125 130 135	
gaa ctc aac aag cct ctg tat gat agg cgg ttt caa atc atc aat gca	724
Glu Leu Asn Lys Pro Leu Tyr Asp Arg Arg Phe Gln Ile Ile Asn Ala	
140 145 150	
gaa tac gag cct aca gaa gaa gaa tgt gaa tgg aat tca gag gat gag	772
Glu Tyr Glu Pro Thr Glu Glu Glu Cys Glu Trp Asn Ser Glu Asp Glu	
155 160 165	
gag ttc agc agt gat gag gag gtg cag gat aac acc cct agt gaa atg	820
Glu Phe Ser Ser Asp Glu Glu Val Gln Asp Asn Thr Pro Ser Glu Met	
170 175 180 185	
cct ccc tta gag ggt gag gaa gaa gaa aac cct aaa gaa aac cca gag	868
Pro Pro Leu Glu Gly Glu Glu Glu Glu Asn Pro Lys Glu Asn Pro Glu	
190 195 200	
gtg aaa gct gaa gag aag gaa gtt cct aaa gaa att cct gag gtg aag	916
Val Lys Ala Glu Glu Lys Glu Val Pro Lys Glu Ile Pro Glu Val Lys	
205 210 215	
gat gaa gaa aag gaa gtt gct aaa gaa att cct gag gta aag gct gaa	964
Asp Glu Glu Lys Glu Val Ala Lys Glu Ile Pro Glu Val Lys Ala Glu	
220 225 230	

gaa aaa gca gat tct aaa gac tgt atg gag gca acc cct gaa gta aaa	1012
Glu Lys Ala Asp Ser Lys Asp Cys Met Glu Ala Thr Pro Glu Val Lys	
235 240 245	
gaa gat cct aaa gaa gtc ccc cag gta aag gca gat gat aaa gaa cag	1060
Glu Asp Pro Lys Glu Val Pro Gln Val Lys Ala Asp Asp Lys Glu Gln	
250 255 260 265	
cct aaa gca aca gag gct aag gca agg gct gca gta aga gag act cat	1108
Pro Lys Ala Thr Glu Ala Lys Ala Arg Ala Ala Val Arg Glu Thr His	
270 275 280	
aaa aga gtt cct gag gaa agg ctt cgg gac agt gta gat ctt aaa aga	1156
Lys Arg Val Pro Glu Glu Arg Leu Arg Asp Ser Val Asp Leu Lys Arg	
285 290 295	
gct agg aag gga aag cct aaa aga gaa gac cct aaa ggc att cct gac	1204
Ala Arg Lys Gly Lys Pro Lys Arg Glu Asp Pro Lys Gly Ile Pro Asp	
300 305 310	
tat tgg ctg att gtt tta aag aat gtt gac aag ctc ggg cct atg att	1252
Tyr Trp Leu Ile Val Leu Lys Asn Val Asp Lys Leu Gly Pro Met Ile	
315 320 325	
cag aag tat gat gag ccc att ctg aag ttc ttg tcg gat gtt agc ctg	1300
Gln Lys Tyr Asp Glu Pro Ile Leu Lys Phe Leu Ser Asp Val Ser Leu	
330 335 340 345	
aag ttc tca aaa cct ggc cag cct gta agt tac acc ttt gaa ttt cat	1348
Lys Phe Ser Lys Pro Gly Gln Pro Val Ser Tyr Thr Phe Glu Phe His	
350 355 360	
ttt cta ccc aac cca tac ttc aga aat gag gtg ctg gtg aag aca tat	1396
Phe Leu Pro Asn Pro Tyr Phe Arg Asn Glu Val Leu Val Lys Thr Tyr	
365 370 375	
ata ata aag gca aaa cca gat cac aat gat ccc ttc ttt tct tgg gga	1444
Ile Ile Lys Ala Lys Pro Asp His Asn Asp Pro Phe Phe Ser Trp Gly	
380 385 390	
tgg gaa att gaa gat tgc aaa ggc tgc aag ata gac cgg aga aga gga	1492
Trp Glu Ile Glu Asp Cys Lys Gly Cys Lys Ile Asp Arg Arg Arg Gly	
395 400 405	
aaa gat gtt act gtg aca act acc cag agt cgc aca act gct act gga	1540
Lys Asp Val Thr Val Thr Thr Thr Gln Ser Arg Thr Thr Ala Thr Gly	
410 415 420 425	
gaa att gaa atc cag cca aga gtg gtt cct aat gca tca ttc ttc aac	1588
Glu Ile Glu Ile Gln Pro Arg Val Val Pro Asn Ala Ser Phe Phe Asn	
430 435 440	
ttc ttt agt cct cct gag att cct atg att ggg aag ctg gaa cca cga	1636
Phe Phe Ser Pro Pro Glu Ile Pro Met Ile Gly Lys Leu Glu Pro Arg	
445 450 455	

Asn Asp Leu Tyr Arg Trp Glu Val Leu Ile Ile Gly Pro Pro Asp Thr  
35 40 45

Leu Tyr Glu Gly Gly Val Phe Lys Ala His Leu Thr Phe Pro Lys Asp  
           50                          55                          60  
 Tyr Pro Leu Arg Pro Pro Lys Met Lys Phe Ile Thr Glu Ile Trp His  
       65                          70                          75                          80  
 Pro Asn Val Asp Lys Asn Gly Asp Val Cys Ile Ser Ile Leu His Glu  
                           85                          90                          95  
 Pro Gly Glu Asp Lys Tyr Gly Tyr Glu Lys Pro Glu Glu Arg Trp Leu  
                   100                          105                          110  
 Pro Ile His Thr Val Glu Thr Ile Met Ile Ser Val Ile Ser Met Leu  
           115                          120                          125  
 Ala Asp Pro Asn Gly Asp Ser Pro Ala Asn Val Asp Ala Ala Lys Glu  
       130                          135                          140  
 Trp Arg Glu Asp Arg Asn Gly Glu Phe Lys Arg Lys Val Ala Arg Cys  
       145                          150                          155                          160  
 Val Arg Lys Ser Gln Glu Thr Ala Phe Glu  
                           165                          170

<210> 23  
 <211> 510  
 <212> DNA  
 <213> Homo sapiens

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 cttattattg gccctccaga tacactttat gaagggtggtg tttttaaggc tcatcttact 180  
 ttcccaaaag attatcccct cgcacctcct aaaatgaaat tcattacaga aatctggcac 240  
 ccaaagtgtg ataaaaatgg tgatgtgtgc atttctattc ttcattgagcc tggggaagat 300  
 aagtatgggt atgaaaagcc agaggaacgc tggctcccta tccacactgt ggaaaccatc 360  
 atgattagtg tcatttctat gctggcagac cctaattggag actcacctgc taatgttgat 420  
 gctgcgaaag aatggagggg agatagaaat ggagaattta aaagaaaagt tgcccgtgtg 480  
 gtaagaaaaa gccaagagac tgcttttgag 510

<210> 24  
 <211> 617  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (19) .. (528)

&lt;400&gt; 24

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      Met Thr Glu Leu Gln Ser Ala Leu Leu Leu Arg
      1          5          10

aga cag ctg gca gaa ctc aac aaa aat cca gtg gaa ggc ttt tct gca 99
Arg Gln Leu Ala Glu Leu Asn Lys Asn Pro Val Glu Gly Phe Ser Ala
      15          20          25

ggt tta ata gat gac aat gat ctc tac cga tgg gaa gtc ctt att att 147
Gly Leu Ile Asp Asp Asn Asp Leu Tyr Arg Trp Glu Val Leu Ile Ile
      30          35          40

ggc cct cca gat aca ctt tat gaa ggt ggt gtt ttt aag gct cat ctt 195
Gly Pro Pro Asp Thr Leu Tyr Glu Gly Gly Val Phe Lys Ala His Leu
      45          50          55

act ttc cca aaa gat tat ccc ctc cga cct cct aaa atg aaa ttc att 243
Thr Phe Pro Lys Asp Tyr Pro Leu Arg Pro Pro Lys Met Lys Phe Ile
      60          65          70          75

aca gaa atc tgg cac cca aat gtt gat aaa aat ggt gat gtg tgc att 291
Thr Glu Ile Trp His Pro Asn Val Asp Lys Asn Gly Asp Val Cys Ile
      80          85          90

tct att ctt cat gag cct ggg gaa gat aag tat ggt tat gaa aag cca 339
Ser Ile Leu His Glu Pro Gly Glu Asp Lys Tyr Gly Tyr Glu Lys Pro
      95          100          105

gag gaa cgc tgg ctc cct atc cac act gtg gaa acc atc atg att agt 387
Glu Glu Arg Trp Leu Pro Ile His Thr Val Glu Thr Ile Met Ile Ser
      110          115          120

gtc att tct atg ctg gca gac cct aat gga gac tca cct gct aat gtt 435
Val Ile Ser Met Leu Ala Asp Pro Asn Gly Asp Ser Pro Ala Asn Val
      125          130          135

gat gct gcg aaa gaa tgg agg gaa gat aga aat gga gaa ttt aaa aga 483
Asp Ala Ala Lys Glu Trp Arg Glu Asp Arg Asn Gly Glu Phe Lys Arg
      140          145          150          155

aaa gtt gcc cgc tgt gta aga aaa agc caa gag act gct ttt gag 528
Lys Val Ala Arg Cys Val Arg Lys Ser Gln Glu Thr Ala Phe Glu
      160          165          170

tgacatttat ttagcagcta gtaacttcac ttatttcagg gtctccaatt gagaaacatg 588

gcactgtttt tctgcactc taccacccg 617

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&lt;210&gt; 25

&lt;211&gt; 374

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 25

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Glu	Gly	Phe	Cys	Trp	Leu	Leu	Leu	Leu	Pro	Val	Met	Leu	Leu	Ile	Val
			20					25					30		
Ala	Arg	Pro	Val	Lys	Leu	Ala	Ala	Phe	Pro	Thr	Ser	Leu	Ser	Asp	Cys
		35					40					45			
Gln	Thr	Pro	Thr	Gly	Trp	Asn	Cys	Ser	Gly	Tyr	Asp	Asp	Arg	Glu	Asn
	50					55					60				
Asp	Leu	Phe	Leu	Cys	Asp	Thr	Asn	Thr	Cys	Lys	Phe	Asp	Gly	Glu	Cys
65					70					75					80
Leu	Arg	Ile	Gly	Asp	Thr	Val	Thr	Cys	Val	Cys	Gln	Phe	Lys	Cys	Asn
				85					90					95	
Asn	Asp	Tyr	Val	Pro	Val	Cys	Gly	Ser	Asn	Gly	Glu	Ser	Tyr	Gln	Asn
			100					105						110	
Glu	Cys	Tyr	Leu	Arg	Gln	Ala	Ala	Cys	Lys	Gln	Gln	Ser	Glu	Ile	Leu
		115					120						125		
Val	Val	Ser	Glu	Gly	Ser	Cys	Ala	Thr	Asp	Ala	Gly	Ser	Gly	Ser	Gly
		130					135				140				
Asp	Gly	Val	His	Glu	Gly	Ser	Gly	Glu	Thr	Ser	Gln	Lys	Glu	Thr	Ser
145					150					155					160
Thr	Cys	Asp	Ile	Cys	Gln	Phe	Gly	Ala	Glu	Cys	Asp	Glu	Asp	Ala	Glu
				165					170					175	
Asp	Val	Trp	Cys	Val	Cys	Asn	Ile	Asp	Cys	Ser	Gln	Thr	Asn	Phe	Asn
			180					185					190		
Pro	Leu	Cys	Ala	Ser	Asp	Gly	Lys	Ser	Tyr	Asp	Asn	Ala	Cys	Gln	Ile
		195					200					205			
Lys	Glu	Ala	Ser	Cys	Gln	Lys	Gln	Glu	Lys	Ile	Glu	Val	Met	Ser	Leu
	210					215					220				
Gly	Arg	Cys	Gln	Asp	Asn	Thr	Thr	Thr	Thr	Thr	Lys	Ser	Glu	Asp	Gly
225					230					235				240	
His	Tyr	Ala	Arg	Thr	Asp	Tyr	Ala	Glu	Asn	Ala	Asn	Lys	Leu	Glu	Glu
				245					250					255	
Ser	Ala	Arg	Glu	His	His	Ile	Pro	Cys	Pro	Glu	His	Tyr	Asn	Gly	Phe
			260					265					270		
Cys	Met	His	Gly	Lys	Cys	Glu	His	Ser	Ile	Asn	Met	Gln	Glu	Pro	Ser
		275					280					285			
Cys	Arg	Cys	Asp	Ala	Gly	Tyr	Thr	Gly	Gln	His	Cys	Glu	Lys	Lys	Asp
	290					295					300				



Tyr Ser Val Leu Tyr Val Val Pro Gly Pro Val Arg Phe Gln Tyr Val  
305 310 315 320

Leu Ile Ala Ala Val Ile Gly Thr Ile Gln Ile Ala Val Ile Cys Val  
325 330 335

Val Val Leu Cys Ile Thr Arg Lys Cys Pro Arg Ser Asn Arg Ile His  
340 345 350

Arg Gln Lys Gln Asn Thr Gly His Tyr Ser Ser Asp Asn Thr Thr Arg  
355 360 365

Ala Ser Thr Arg Leu Ile  
370

<210> 26

<211> 1122

<212> DNA

<213> Homo sapiens

<400> 26

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ttccctacct ccttaagtga ctgccaaacg cccaccggct ggaattgctc tggttatgat 180  
gacagagaaa atgatctctt cctctgtgac accaacacct gttaaatttga tggggaatgt 240  
ttaagaattg gagacactgt gacttgctgc tgtcagttca agtgcaacaa tgactatgtg 300  
cctgtgtgtg gctccaatgg ggagagctac cagaatgagt gttacctgcg acaggctgca 360  
tgcaaacagc agagtgagat acttgtggtg tcagaaggat catgtgccac agatgcagga 420  
tcaggatctg gagatggagt ccatgaaggc tctggagaaa ctagtcaaaa ggagacatcc 480  
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caccacatac cttgtccgga acattacaat ggcttctgca tgcattggaa gtgtgagcat 840  
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gaaaaaaaagg actacagtgt tctatacgtt gttcccggtc ctgtacgatt tcagtatgtc 960  
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atcacaagga aatgccccag aagcaacaga attcacagac agaagcaaaa tacagggcac 1080

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1122

<210> 27  
 <211> 1721  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (368)..(1489)

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 cccgcgtctc cggcgcagct tctcagcgga cgacctctc gctccggggc tgagccagtc 180  
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 gtgccactgc caccgcgcgc gcctctgctg ccgccgtccg cgggatgctc agtagcccg 300  
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 Met Val Leu Trp Glu Ser Pro Arg Gln Cys Ser Ser Trp Thr  
 1 5 10  
 ctt tgc gag ggc ttt tgc tgg ctg ctg ctg ctg ccc gtc atg cta ctc 457  
 Leu Cys Glu Gly Phe Cys Trp Leu Leu Leu Leu Pro Val Met Leu Leu  
 15 20 25 30  
 atc gta gcc cgc ccg gtg aag ctc gct gct ttc cct acc tcc tta agt 505  
 Ile Val Ala Arg Pro Val Lys Leu Ala Ala Phe Pro Thr Ser Leu Ser  
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 gac tgc caa acg ccc acc ggc tgg aat tgc tct ggt tat gat gat aga 553  
 Asp Cys Gln Thr Pro Thr Gly Trp Asn Cys Ser Gly Tyr Asp Asp Arg  
 50 55 60  
 gaa aat gat ctc ttc ctc tgt gac acc aac acc tgt aaa ttt gat ggg 601  
 Glu Asn Asp Leu Phe Leu Cys Asp Thr Asn Thr Cys Lys Phe Asp Gly  
 65 70 75  
 gaa tgt tta aga att gga gac act gtg act tgc gtc tgt cag ttc aag 649  
 Glu Cys Leu Arg Ile Gly Asp Thr Val Thr Cys Val Cys Gln Phe Lys  
 80 85 90  
 tgc aac aat gac tat gtg cct gtg tgt ggc tcc aat ggg gag agc tac 697  
 Cys Asn Asn Asp Tyr Val Pro Val Cys Gly Ser Asn Gly Glu Ser Tyr  
 95 100 105 110  
 cag aat gag tgt tac ctg cga cag gct gca tgc aaa cag cag agt gag 745  
 Gln Asn Glu Cys Tyr Leu Arg Gln Ala Ala Cys Lys Gln Gln Ser Glu  
 115 120 125

ata ctt gtg gtg tca gaa gga tca tgt gcc aca gat gca gga tca gga Ile Leu Val Val Ser Glu Gly Ser Cys Ala Thr Asp Ala Gly Ser Gly 130 135 140	793
tct gga gat gga gtc cat gaa ggc tct gga gaa act agt caa aag gag Ser Gly Asp Gly Val His Glu Gly Ser Gly Glu Thr Ser Gln Lys Glu 145 150 155	841
aca tcc acc tgt gat att tgc cag ttt ggt gca gaa tgt gac gaa gat Thr Ser Thr Cys Asp Ile Cys Gln Phe Gly Ala Glu Cys Asp Glu Asp 160 165 170	889
gcc gag gat gtc tgg tgt gtg tgt aat att gac tgt tct caa acc aac Ala Glu Asp Val Trp Cys Val Cys Asn Ile Asp Cys Ser Gln Thr Asn 175 180 185 190	937
ttc aat ccc ctc tgc gct tct gat ggg aaa tct tat gat aat gca tgc Phe Asn Pro Leu Cys Ala Ser Asp Gly Lys Ser Tyr Asp Asn Ala Cys 195 200 205	985
caa atc aaa gaa gca tgc tgt cag aaa cag gag aaa att gaa gtc atg Gln Ile Lys Glu Ala Ser Cys Gln Lys Gln Glu Lys Ile Glu Val Met 210 215 220	1033
tct ttg ggt cga tgt caa gat aac aca act aca act act aag tct gaa Ser Leu Gly Arg Cys Gln Asp Asn Thr Thr Thr Thr Lys Ser Glu 225 230 235	1081
gat ggg cat tat gca aga aca gat tat gca gag aat gct aac aaa tta Asp Gly His Tyr Ala Arg Thr Asp Tyr Ala Glu Asn Ala Asn Lys Leu 240 245 250	1129
gaa gaa agt gcc aga gaa cac cac ata cct tgt ccg gaa cat tac aat Glu Glu Ser Ala Arg Glu His His Ile Pro Cys Pro Glu His Tyr Asn 255 260 265 270	1177
ggc ttc tgc atg cat ggg aag tgt gag cat tct atc aat atg cag gag Gly Phe Cys Met His Gly Lys Cys Glu His Ser Ile Asn Met Gln Glu 275 280 285	1225
cca tct tgc agg tgt gat gct ggt tat act gga caa cac tgt gaa aaa Pro Ser Cys Arg Cys Asp Ala Gly Tyr Thr Gly Gln His Cys Glu Lys 290 295 300	1273
aag gac tac agt gtt cta tac gtt gtt ccc ggt cct gta cga ttt cag Lys Asp Tyr Ser Val Leu Tyr Val Val Pro Gly Pro Val Arg Phe Gln 305 310 315	1321
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tgt gtg gtg gtc ctc tgc atc aca agg aaa tgc ccc aga agc aac aga Cys Val Val Val Leu Cys Ile Thr Arg Lys Cys Pro Arg Ser Asn Arg 335 340 345 350	1417

att cac aga cag aag caa aat aca ggg cac tac agt tca gac aat aca 1465  
 Ile His Arg Gln Lys Gln Asn Thr Gly His Tyr Ser Ser Asp Asn Thr  
                   355                                  360                                  365

aca aga gcg tcc acg agg tta atc taaagggagc atgtttcaca gtggctggac 1519  
 Thr Arg Ala Ser Thr Arg Leu Ile  
                   370

taccgagagc ttggactaca caatacagta ttatagacaa aagaataaga caagagatct 1579  
 acacatgttg ccttgcatTT gtggtaatct acaccaatga aaacatgtac tacagctata 1639  
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<211> 817

<212> PRT

<213> Homo sapiens

<400> 28

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Ile Thr Glu Gly Val Gly Glu Leu Ser Val Ile Asp Pro Glu Val Ala  
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Gln Lys Ala Cys Gln Glu Val Leu Glu Lys Val Lys Leu Leu His Gly  
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Gly Val Ala Val Ser Ser Arg Gly Thr Pro Leu Glu Leu Val Asn Gly  
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Asp Gly Val Asp Ser Glu Ile Arg Cys Leu Asp Asp Pro Pro Ala Gln  
                                   85                                  90                                  95

Ile Arg Glu Glu Glu Asp Glu Met Gly Ala Ala Val Ala Ser Gly Thr  
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Ala Lys Gly Ala Arg Arg Arg Arg Gln Asn Asn Ser Ala Lys Gln Ser  
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Trp Leu Leu Arg Leu Phe Glu Ser Lys Leu Phe Asp Ile Ser Met Ala  
                   130                                  135                                  140

Ile Ser Tyr Leu Tyr Asn Ser Lys Glu Pro Gly Val Gln Ala Tyr Ile  
                   145                                  150                                  155                                  160

Gly Asn Arg Leu Phe Cys Phe Arg Asn Glu Asp Val Asp Phe Tyr Leu  
                                   165                                  170                                  175

Pro Gln Leu Leu Asn Met Tyr Ile His Met Asp Glu Asp Val Gly Asp  
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Ala Ile Lys Pro Tyr Ile Val His Arg Cys Arg Gln Ser Ile Asn Phe  
 195 200 205  
 Ser Leu Gln Cys Ala Leu Leu Leu Gly Ala Tyr Ser Ser Asp Met His  
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 Ile Ser Thr Gln Arg His Ser Arg Gly Thr Lys Leu Arg Lys Leu Ile  
 225 230 235 240  
 Leu Ser Asp Glu Leu Lys Pro Ala His Arg Lys Arg Glu Leu Pro Ser  
 245 250 255  
 Leu Ser Pro Ala Pro Asp Thr Gly Leu Ser Pro Ser Lys Arg Thr His  
 260 265 270  
 Gln Arg Ser Lys Ser Asp Ala Thr Ala Ser Ile Ser Leu Ser Ser Asn  
 275 280 285  
 Leu Lys Arg Thr Ala Ser Asn Pro Lys Val Glu Asn Glu Asp Glu Glu  
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 Leu Ser Ser Ser Thr Glu Ser Ile Asp Asn Ser Phe Ser Ser Pro Val  
 305 310 315 320  
 Arg Leu Ala Pro Glu Arg Glu Phe Ile Lys Ser Leu Met Ala Ile Gly  
 325 330 335  
 Lys Arg Leu Ala Thr Leu Pro Thr Lys Glu Gln Lys Thr Gln Arg Leu  
 340 345 350  
 Ile Ser Glu Leu Ser Leu Leu Asn His Lys Leu Pro Ala Arg Val Trp  
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 Leu Pro Thr Ala Gly Phe Asp His His Val Val Arg Val Pro His Thr  
 370 375 380  
 Gln Ala Val Val Leu Asn Ser Lys Asp Lys Ala Pro Tyr Leu Ile Tyr  
 385 390 395 400  
 Val Glu Val Leu Glu Cys Glu Asn Phe Asp Thr Thr Ser Val Pro Ala  
 405 410 415  
 Arg Ile Pro Glu Asn Arg Ile Arg Ser Thr Arg Ser Val Glu Asn Leu  
 420 425 430  
 Pro Glu Cys Gly Ile Thr His Glu Gln Arg Ala Gly Ser Phe Ser Thr  
 435 440 445  
 Val Pro Asn Tyr Asp Asn Asp Asp Glu Ala Trp Ser Val Asp Asp Ile  
 450 455 460  
 Gly Glu Leu Gln Val Glu Leu Pro Glu Val His Thr Asn Ser Cys Asp  
 465 470 475 480  
 Asn Ile Ser Gln Phe Ser Val Asp Ser Ile Thr Ser Gln Glu Ser Lys  
 485 490 495

Glu Pro Val Phe Ile Ala Ala Gly Asp Ile Arg Arg Arg Leu Ser Glu  
 500 505 510  
 Gln Leu Ala His Thr Pro Thr Ala Phe Lys Arg Asp Pro Glu Asp Pro  
 515 520 525  
 Ser Ala Val Ala Leu Lys Glu Pro Trp Gln Glu Lys Val Arg Arg Ile  
 530 535 540  
 Arg Glu Gly Ser Pro Tyr Gly His Leu Pro Asn Trp Arg Leu Leu Ser  
 545 550 555 560  
 Val Ile Val Lys Cys Gly Asp Asp Leu Arg Gln Glu Leu Leu Ala Phe  
 565 570 575  
 Gln Val Leu Lys Gln Leu Gln Ser Ile Trp Glu Gln Glu Arg Val Pro  
 580 585 590  
 Leu Trp Ile Lys Pro Ile Gln Asp Ser Cys Glu Ile Thr Thr Asp Ser  
 595 600 605  
 Gly Met Ile Glu Pro Val Val Asn Ala Val Ser Ile His Gln Val Lys  
 610 615 620  
 Lys Gln Ser Gln Leu Ser Leu Leu Asp Tyr Phe Leu Gln Glu His Gly  
 625 630 635 640  
 Ser Tyr Thr Thr Glu Ala Phe Leu Ser Ala Gln Arg Asn Phe Val Gln  
 645 650 655  
 Ser Cys Ala Gly Tyr Cys Leu Val Cys Tyr Leu Leu Gln Val Lys Asp  
 660 665 670  
 Arg His Asn Gly Asn Ile Leu Leu Asp Ala Glu Gly His Ile Ile His  
 675 680 685  
 Ile Asp Phe Gly Phe Ile Leu Ser Ser Ser Pro Arg Asn Leu Gly Phe  
 690 695 700  
 Glu Thr Ser Ala Phe Lys Leu Thr Thr Glu Phe Val Asp Val Met Gly  
 705 710 715 720  
 Gly Leu Asp Gly Asp Met Phe Asn Tyr Tyr Lys Met Leu Met Leu Gln  
 725 730 735  
 Gly Leu Ile Ala Ala Arg Lys His Met Asp Lys Val Val Gln Ile Val  
 740 745 750  
 Glu Ile Met Gln Gln Gly Ser Gln Leu Pro Cys Phe His Gly Ser Ser  
 755 760 765  
 Thr Ile Arg Asn Leu Lys Glu Arg Phe His Met Ser Met Thr Glu Glu  
 770 775 780  
 Gln Leu Gln Leu Leu Val Glu Gln Met Val Asp Gly Ser Met Arg Ser  
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<211> 2451

<212> DNA

<213> Homo sapiens

<400> 29

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 cttttgcatg gaggcgtggc agtctctagc agaggcacc cactggagtt ggtcaatggg 240  
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 atctccatgg ccatttcata cctgtataac tccaaggagc ctggagtaca agcctacatt 480  
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<211> 3602

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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<400> 30

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accgcgactg cccgcacccc ctccgcgggg tccccagag cttggaagct cgaagtctgg 420  
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         1                    5                    10  
 tct gag ccc act tct ggc cca cca ggg aat aat ggg ggg tcc ctg cta 518  
 Ser Glu Pro Thr Ser Gly Pro Pro Gly Asn Asn Gly Gly Ser Leu Leu  
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 agt gtc atc acg gag ggg gtc ggg gaa cta tca gtg att gac cct gag 566  
 Ser Val Ile Thr Glu Gly Val Gly Glu Leu Ser Val Ile Asp Pro Glu  
                 35                    40                    45  
 gtg gcc cag aag gcc tgc cag gag gtg ttg gag aaa gtc aag ctt ttg 614  
 Val Ala Gln Lys Ala Cys Gln Glu Val Leu Glu Lys Val Lys Leu Leu  
                 50                    55                    60  
 cat gga ggc gtg gca gtc tct agc aga ggc acc cca ctg gag ttg gtc 662  
 His Gly Gly Val Ala Val Ser Ser Arg Gly Thr Pro Leu Glu Leu Val  
         65                    70                    75  
 aat ggg gat ggt gtg gac agt gag atc cgt tgc cta gat gat cca cct 710  
 Asn Gly Asp Gly Val Asp Ser Glu Ile Arg Cys Leu Asp Asp Pro Pro  
         80                    85                    90  
 gcc cag atc agg gag gag gaa gat gag atg ggg gcc gct gtg gcc tca 758  
 Ala Gln Ile Arg Glu Glu Glu Asp Glu Met Gly Ala Ala Val Ala Ser  
         95                    100                    105                    110  
 ggc aca gcc aaa gga gca aga aga cgg cgg cag aac aac tca gct aaa 806  
 Gly Thr Ala Lys Gly Ala Arg Arg Arg Arg Gln Asn Asn Ser Ala Lys  
                 115                    120                    125  
 cag tct tgg ctg ctg agg ctg ttt gag tca aaa ctg ttt gac atc tcc 854  
 Gln Ser Trp Leu Leu Arg Leu Phe Glu Ser Lys Leu Phe Asp Ile Ser  
                 130                    135                    140  
 atg gcc att tca tac ctg tat aac tcc aag gag cct gga gta caa gcc 902  
 Met Ala Ile Ser Tyr Leu Tyr Asn Ser Lys Glu Pro Gly Val Gln Ala  
                 145                    150                    155  
 tac att ggc aac cgg ctc ttc tgc ttt cgc aac gag gac gtg gac ttc 950  
 Tyr Ile Gly Asn Arg Leu Phe Cys Phe Arg Asn Glu Asp Val Asp Phe  
         160                    165                    170  
 tat ctg ccc cag ttg ctt aac atg tac atc cac atg gat gag gac gtg 998  
 Tyr Leu Pro Gln Leu Leu Asn Met Tyr Ile His Met Asp Glu Asp Val  
         175                    180                    185                    190  
 ggt gat gcc att aag ccc tac ata gtc cac cgt tgc cgc cag agc att 1046  
 Gly Asp Ala Ile Lys Pro Tyr Ile Val His Arg Cys Arg Gln Ser Ile  
                 195                    200                    205  
 aac ttt tcc ctc cag tgt gcc ctg ttg ctt ggg gcc tat tct tca gac 1094  
 Asn Phe Ser Leu Gln Cys Ala Leu Leu Leu Gly Ala Tyr Ser Ser Asp  
                 210                    215                    220

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Met His Ile Ser Thr Gln Arg His Ser Arg Gly Thr Lys Leu Arg Lys	
225 230 235	
ctg atc ctc tca gat gag cta aag cca gct cac agg aag agg gag ctg	1190
Leu Ile Leu Ser Asp Glu Leu Lys Pro Ala His Arg Lys Arg Glu Leu	
240 245 250	
ccc tcc ttg agc ccg gcc cct gat aca ggg ctg tct ccc tcc aaa agg	1238
Pro Ser Leu Ser Pro Ala Pro Asp Thr Gly Leu Ser Pro Ser Lys Arg	
255 260 265 270	
act cac cag cgc tct aag tca gat gcc act gcc agc ata agt ctc agc	1286
Thr His Gln Arg Ser Lys Ser Asp Ala Thr Ala Ser Ile Ser Leu Ser	
275 280 285	
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Ser Asn Leu Lys Arg Thr Ala Ser Asn Pro Lys Val Glu Asn Glu Asp	
290 295 300	
gag gag ctc tcc tcc agc acc gag agt att gat aat tca ttc agt tcc	1382
Glu Glu Leu Ser Ser Ser Thr Glu Ser Ile Asp Asn Ser Phe Ser Ser	
305 310 315	
cct gtt cga ctg gct cct gag aga gaa ttc atc aag tcc ctg atg gcg	1430
Pro Val Arg Leu Ala Pro Glu Arg Glu Phe Ile Lys Ser Leu Met Ala	
320 325 330	
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Ile Gly Lys Arg Leu Ala Thr Leu Pro Thr Lys Glu Gln Lys Thr Gln	
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Arg Leu Ile Ser Glu Leu Ser Leu Leu Asn His Lys Leu Pro Ala Arg	
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Val Trp Leu Pro Thr Ala Gly Phe Asp His His Val Val Arg Val Pro	
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His Thr Gln Ala Val Val Leu Asn Ser Lys Asp Lys Ala Pro Tyr Leu	
385 390 395	
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Ile Tyr Val Glu Val Leu Glu Cys Glu Asn Phe Asp Thr Thr Ser Val	
400 405 410	
cct gcc cgg atc ccc gag aac cga att cgg agt acg agg tcc gta gaa	1718
Pro Ala Arg Ile Pro Glu Asn Arg Ile Arg Ser Thr Arg Ser Val Glu	
415 420 425 430	
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Asn Leu Pro Glu Cys Gly Ile Thr His Glu Gln Arg Ala Gly Ser Phe	
435 440 445	

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Ser Thr Val Pro Asn Tyr Asp Asn Asp Asp Glu Ala Trp Ser Val Asp	
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Cys Asp Asn Ile Ser Gln Phe Ser Val Asp Ser Ile Thr Ser Gln Glu	
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Ser Lys Glu Pro Val Phe Ile Ala Ala Gly Asp Ile Arg Arg Arg Leu	
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Ser Glu Gln Leu Ala His Thr Pro Thr Ala Phe Lys Arg Asp Pro Glu	
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Asp Pro Ser Ala Val Ala Leu Lys Glu Pro Trp Gln Glu Lys Val Arg	
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Arg Ile Arg Glu Gly Ser Pro Tyr Gly His Leu Pro Asn Trp Arg Leu	
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Ala Phe Gln Val Leu Lys Gln Leu Gln Ser Ile Trp Glu Gln Glu Arg	
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Val Pro Leu Trp Ile Lys Pro Ile Gln Asp Ser Cys Glu Ile Thr Thr	
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625 630 635	
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His Gly Ser Tyr Thr Thr Glu Ala Phe Leu Ser Ala Gln Arg Asn Phe	
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655 660 665 670	

aag gac aga cac aat ggg aat atc ctt ttg gac gca gaa ggc cac atc 2486  
Lys Asp Arg His Asn Gly Asn Ile Leu Leu Asp Ala Glu Gly His Ile  
675 680 685

atc cac atc gac ttt ggc ttc atc ctc tcc agc tca ccc cga aat ctg 2534  
Ile His Ile Asp Phe Gly Phe Ile Leu Ser Ser Ser Pro Arg Asn Leu  
690 695 700

ggc ttt gag acg tca gcc ttt aag ctg acc aca gag ttt gtg gat gtg 2582  
Gly Phe Glu Thr Ser Ala Phe Lys Leu Thr Thr Glu Phe Val Asp Val  
705 710 715

atg ggc ggc ctg gat ggc gac atg ttc aac tac tat aag atg ctg atg 2630  
Met Gly Gly Leu Asp Gly Asp Met Phe Asn Tyr Tyr Lys Met Leu Met  
720 725 730

ctg caa ggg ctg att gcc gct cgg aaa cac atg gac aag gtg gtg cag 2678  
Leu Gln Gly Leu Ile Ala Ala Arg Lys His Met Asp Lys Val Val Gln  
735 740 745 750

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755 760 765

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Ser Ser Thr Ile Arg Asn Leu Lys Glu Arg Phe His Met Ser Met Thr  
770 775 780

gag gag cag ctg cag ctg ctg gtg gag cag atg gtg gat ggc agt atg 2822  
Glu Glu Gln Leu Gln Leu Leu Val Glu Gln Met Val Asp Gly Ser Met  
785 790 795

cgg tct atc acc acc aaa ctc tat gac ggc ttc cag tac ctc acc aac 2870  
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ggc atc atg tgacacgctc ctcagcccag gagggtggg ggggccaggg 2919  
Gly Ile Met  
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 Gln Glu Val Leu Glu Lys Val Lys Leu Leu His Gly Gly Val Ala Val  
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           100                  105                  110  
 Glu Asp Glu Met Gly Ala Ala Val Ala Ser Gly Thr Ala Lys Gly Ala  
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 Phe Cys Phe Arg Asn Glu Asp Val Asp Phe Tyr Leu Pro Gln Leu Leu  
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 Thr Leu Pro Thr Lys Glu Gln Lys Thr Gln Arg Leu Ile Ser Glu Leu  
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 Glu Cys Glu Asn Phe Asp Thr Thr Ser Val Pro Ala Arg Ile Pro Glu  
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 Gln Leu Gln Ser Ile Trp Glu Gln Glu Arg Val Pro Leu Trp Ile Lys  
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 Pro Ile Gln Asp Ser Cys Glu Ile Thr Thr Asp Ser Gly Met Ile Glu  
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 Gln Gly Ser Gln Leu Pro Cys Phe His Gly Ser Ser Thr Ile Arg Asn  
 770 775 780  
 Leu Lys Glu Arg Phe His Met Ser Met Thr Glu Glu Gln Leu Gln Leu  
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 Val Glu Pro Ala Pro Leu Lys Pro Thr Ser Glu Pro Thr Ser Gly Pro  
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Asp Thr Gly Leu Ser Pro Ser Lys Arg Thr His Gln Arg Ser Lys Ser	
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Asn Ser Lys Asp Lys Ala Pro Tyr Leu Ile Tyr Val Glu Val Leu Glu	
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Thr His Glu Gln Arg Ala Gly Ser Phe Ser Thr Val Pro Asn Tyr Asp	
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Asn Asp Asp Glu Ala Trp Ser Val Asp Asp Ile Gly Glu Leu Gln Val	
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Glu Leu Pro Glu Val His Thr Asn Ser Cys Asp Asn Ile Ser Gln Phe	
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Gly Ser Gln Leu Pro Cys Phe His Gly Ser Ser Thr Ile Arg Asn Leu  
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aaa gag agg ttc cac atg agc atg act gag gag cag ctg cag ctg ctg 2517  
Lys Glu Arg Phe His Met Ser Met Thr Glu Glu Gln Leu Gln Leu Leu  
790 795 800

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Val Glu Gln Met Val Asp Gly Ser Met Arg Ser Ile Thr Thr Lys Leu  
805 810 815

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Tyr Asp Gly Phe Gln Tyr Leu Thr Asn Gly Ile Met  
820 825

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 100 105 110  
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 Pro Pro Asp Thr Asn Leu Pro Pro Gly Ile Asn Leu Trp Leu Gly Gln  
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 Arg Asn Gln Lys His Gly Leu Phe Lys Gly Ile Ile Gln Asp Gly Lys  
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 His Thr Cys Pro Thr Cys Ser Asp Phe Leu Ser Leu Val Gln Gly Ile  
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 Cys Gln Val Ser Gly Leu Leu Tyr Arg Asp Gln Asp Ser Trp Val Asp  
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 Tyr Gly Gly Lys Val Leu Ala Glu Gly Gln Arg Ile Leu Thr Lys Ser  
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 Cys Arg Glu Cys Arg Gly Gly Val Leu Val Lys Ile Thr Glu Met Cys  
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 Glu Cys Lys Ser Gly Tyr Ile Ser Val Gln Gly Asp Ser Ala Tyr Cys  
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 Val Gln Gly His Ser Cys Thr Cys Lys Pro Gly Tyr Val Gly Asn Gly  
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 His Asn His Ser Arg Cys Val Asn Leu Pro Gly Trp Tyr His Cys Glu  
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 Cys Arg Ser Gly Phe His Asp Asp Gly Thr Tyr Ser Leu Ser Gly Glu  
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 Ser Cys Ile Asp Ile Asp Glu Cys Ala Leu Arg Thr His Thr Cys Trp  
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 Cys Gln Asn Pro Ser Ala Asp Leu Phe Cys Cys Pro Glu Cys Asp Thr  
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<211> 2430

<212> DNA

<213> Homo sapiens

<400> 35

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tatgacatca gaaaaacttg cctggacagc tatggtgttt cacggcttag tggctcagtg 2340
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<210> 36

<211> 2977

<212> DNA

<213> Homo sapiens

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<222> (103)..(2532)

<400> 36

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                                     Met Pro Met Asp
                                     1

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Leu Ile Leu Val Val Trp Phe Cys Val Cys Thr Ala Arg Thr Val Val
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ggc ttt ggg atg gac cct gac ctt cag atg gat atc gtc acc gag ctt      210
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gac ctt gtg aac acc acc ctt gga gtt gct cag gtg tct gga atg cac      258
Asp Leu Val Asn Thr Thr Leu Gly Val Ala Gln Val Ser Gly Met His
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aat gcc agc aaa gca ttt tta ttt caa gac ata gaa aga gag atc cat      306
Asn Ala Ser Lys Ala Phe Leu Phe Gln Asp Ile Glu Arg Glu Ile His
                               55                               60                               65

gca gct cct cat gtg agt gag aaa tta att cag ctg ttc cag aac aag      354
Ala Ala Pro His Val Ser Glu Lys Leu Ile Gln Leu Phe Gln Asn Lys
   70                               75                               80

agt gaa ttc acc att ttg gcc act gta cag cag aag cca tcc act tca      402
Ser Glu Phe Thr Ile Leu Ala Thr Val Gln Gln Lys Pro Ser Thr Ser
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gga gtg ata ctg tcc att cga gaa ctg gag cac agc tat ttt gaa ctg      450
Gly Val Ile Leu Ser Ile Arg Glu Leu Glu His Ser Tyr Phe Glu Leu
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Glu Ser Ser Gly Leu Arg Asp Glu Ile Arg Tyr His Tyr Ile His Asn	
120 125 130	
ggg aag cca agg aca gag gca ctt cct tac cgc atg gca gat gga caa	546
Gly Lys Pro Arg Thr Glu Ala Leu Pro Tyr Arg Met Ala Asp Gly Gln	
135 140 145	
tgg cac aag gtt gca ctg tca gtt agc gcc tct cat ctc ctg ctc cat	594
Trp His Lys Val Ala Leu Ser Val Ser Ala Ser His Leu Leu Leu His	
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gtc gac tgt aac agg att tat gag cgt gtg ata gac cct cca gat acc	642
Val Asp Cys Asn Arg Ile Tyr Glu Arg Val Ile Asp Pro Pro Asp Thr	
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Asn Leu Pro Pro Gly Ile Asn Leu Trp Leu Gly Gln Arg Asn Gln Lys	
185 190 195	
cat ggc tta ttc aaa ggg atc atc caa gat ggg aag atc atc ttt atg	738
His Gly Leu Phe Lys Gly Ile Ile Gln Asp Gly Lys Ile Ile Phe Met	
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ccg aat gga tat ata aca cag tgt cca aat cta aat cac act tgc cca	786
Pro Asn Gly Tyr Ile Thr Gln Cys Pro Asn Leu Asn His Thr Cys Pro	
215 220 225	
acc tgc agt gat ttc tta agc ctg gtg caa gga ata atg gat tta caa	834
Thr Cys Ser Asp Phe Leu Ser Leu Val Gln Gly Ile Met Asp Leu Gln	
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gag ctt ttg gcc aag atg act gca aaa cta aat tat gca gag aca aga	882
Glu Leu Leu Ala Lys Met Thr Ala Lys Leu Asn Tyr Ala Glu Thr Arg	
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Leu Ser Gln Leu Glu Asn Cys His Cys Glu Lys Thr Cys Gln Val Ser	
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Gly Leu Leu Tyr Arg Asp Gln Asp Ser Trp Val Asp Gly Asp His Cys	
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agg aac tgc act tgc aaa agt ggt gcc gtg gaa tgc cga agg atg tcc	1026
Arg Asn Cys Thr Cys Lys Ser Gly Ala Val Glu Cys Arg Arg Met Ser	
295 300 305	
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Cys Pro Pro Leu Asn Cys Ser Pro Asp Ser Leu Pro Val His Ile Ala	
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Arg Gly Gly Val Leu Val Lys Ile Thr Glu Met Cys Pro Pro Leu Asn	
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Cys Ser Glu Lys Asp His Ile Leu Pro Glu Asn Gln Cys Cys Arg Val	
375 380 385	
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Cys Arg Gly His Asn Phe Cys Ala Glu Gly Pro Lys Cys Gly Glu Asn	
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Ser Glu Cys Lys Asn Trp Asn Thr Lys Ala Thr Cys Glu Cys Lys Ser	
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His Asn Cys Asp Glu Asn Ala Ile Cys Thr Asn Thr Val Gln Gly His	
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Asn Lys Cys Val Cys Pro Ser Gly Phe Thr Gly Ser His Cys Glu Lys	
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gat att gat gaa tgt tca gag gga atc att gag tgc cac aac cat tcc	1794
Asp Ile Asp Glu Cys Ser Glu Gly Ile Ile Glu Cys His Asn His Ser	
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Arg Cys Val Asn Leu Pro Gly Trp Tyr His Cys Glu Cys Arg Ser Gly	
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Phe His Asp Asp Gly Thr Tyr Ser Leu Ser Gly Glu Ser Cys Ile Asp	
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Ile Asp Glu Cys Ala Leu Arg Thr His Thr Cys Trp Asn Asp Ser Ala	
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Cys Ile Asn Leu Ala Gly Gly Phe Asp Cys Leu Cys Pro Ser Gly Pro	
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760 765 770	
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 Glu Cys Leu Gln Asn Asn  
 805 810

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Arg Ser Ile Lys Ala Ser Thr Ala Thr Ala Glu Gln Phe Phe Gln Lys  
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Leu Arg Asn Lys His Glu Phe Thr Ile Leu Val Thr Leu Lys Gln Thr  
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His Leu Asn Ser Gly Val Ile Leu Ser Ile His His Leu Asp His Arg  
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Tyr Leu Glu Leu Glu Ser Ser Gly His Arg Asn Glu Val Arg Leu His  
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Tyr Arg Ser Gly Ser His Arg Pro His Thr Glu Val Phe Pro Tyr Ile  
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 595 600 605  
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 Gly Tyr Asp Cys Arg Cys Pro His Gly Lys Asn Cys Thr Gly Asp Cys  
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 Ile His Asp Gly Lys Val Lys His Asn Gly Gln Ile Trp Val Leu Glu  
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 Pro Arg Cys Val Thr Asp Pro Cys Gln Ala Asp Thr Ile Arg Asn Asp  
 755 760 765



Ile Thr Lys Thr Cys Leu Asp Glu Met Asn Val Val Arg Phe Thr Gly  
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Ser Ser Trp Ile Lys His Gly Thr Glu Cys Thr Leu Cys Gln Cys Lys  
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<210> 38

<211> 2448

<212> DNA

<213> Homo sapiens

<400> 38

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 act gtg gtc ctg gga aag ctg gaa tcc ggg tcc att ttt aaa ggc cag	1133
Thr Val Val Leu Gly Lys Leu Glu Ser Gly Ser Ile Phe Lys Gly Gln	
315 320 325 330	
 cag ctc gtg atg atg cca aac aag cac aat gta gaa gtt ctt gga ata	1181
Gln Leu Val Met Met Pro Asn Lys His Asn Val Glu Val Leu Gly Ile	
335 340 345	
 ctt tct gat gat act gaa act gat ttt gta gcc cca ggt gaa aac ctc	1229
Leu Ser Asp Asp Thr Glu Thr Asp Phe Val Ala Pro Gly Glu Asn Leu	
350 355 360	
 aaa atc aga ctg aag gga att gaa gaa gaa gag att ctt cca gaa ttc	1277
Lys Ile Arg Leu Lys Gly Ile Glu Glu Glu Glu Ile Leu Pro Glu Phe	
365 370 375	
 ata ctt tgt gat cct agt aac ctc tgc cat tct gga cgc acg ttt gat	1325
Ile Leu Cys Asp Pro Ser Asn Leu Cys His Ser Gly Arg Thr Phe Asp	
380 385 390	
 gtt cag ata gtg att att gag cac aaa tcc atc atc tgc cca ggt tat	1373
Val Gln Ile Val Ile Ile Glu His Lys Ser Ile Ile Cys Pro Gly Tyr	
395 400 405 410	
 aat gcg gtg ctg cac att cat act tgt att gag gaa gtt gag ata aca	1421
Asn Ala Val Leu His Ile His Thr Cys Ile Glu Glu Val Glu Ile Thr	
415 420 425	
 gcg tta atc tcc ttg gta gac aaa aaa tca ggg gaa aaa agt aag aca	1469
Ala Leu Ile Ser Leu Val Asp Lys Lys Ser Gly Glu Lys Ser Lys Thr	
430 435 440	

cga ccc cgc ttc gtg aaa caa gat caa gta tgc att gct cgt tta agg 1517  
 Arg Pro Arg Phe Val Lys Gln Asp Gln Val Cys Ile Ala Arg Leu Arg  
           445                          450                          455

aca gca gga acc atc tgc ctc gag acg ttc aaa gat ttt cct cag atg 1565  
 Thr Ala Gly Thr Ile Cys Leu Glu Thr Phe Lys Asp Phe Pro Gln Met  
           460                          465                          470

ggc cgt ttt act tta aga gat gag ggt aag acc att gca att gga aaa 1613  
 Gly Arg Phe Thr Leu Arg Asp Glu Gly Lys Thr Ile Ala Ile Gly Lys  
           475                          480                          485                          490

gtt ctg aaa ttg gtc cca gag aag gac taagcaattt tcttgatgcc 1660  
 Val Leu Lys Leu Val Pro Glu Lys Asp  
   495

tctgcaagat actgtgagga gaattgacag caaaagttca ccacctactc ttatttactg 1720  
 cccattgatt gactttttctt catattttgc aaagagaaat ttcacagcaa aaattcatgt 1780  
 tttgtcagct ttctcatgtt gagatctggt atgtcactga tgaatttacc ctcaagtttc 1840  
 cttcctctgt accactctgc ttccttggac aatatcagta atagctttgt aagtgatgtg 1900  
 gacgtaattg cctacagtaa taaaaaaata atgtacttta atttttcatt ttcttttagg 1960  
 atatttagac cacccttggt ccacgcaaac cagagtgtgt cagtgtttgt gtgtgtgtta 2020  
 aaatgataac taacatgtga ataaaatact ccatttg 2057

<210> 43

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer P1

<400> 43

acaccaatcc agtagccagg cttg

24

<210> 44

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer P2

<400> 44

cactcgagaa tctgtgagac ctacatacat gacg

34

<210> 45

<211> 21

<212> PRT

## &lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: consensus  
sequence

&lt;220&gt;

&lt;223&gt; all "Xaa" amino acids are unidentified

&lt;400&gt; 45

Cys	Xaa	Glu	Cys	Gly	Lys	Ala	Phe	Xaa	Gln	Lys	Ser	Xaa	Leu	Xaa	Xaa
1				5					10					15	

His	Gln	Arg	Xaa	His
				20

&lt;210&gt; 46

&lt;211&gt; 7

&lt;212&gt; PRT

&lt;213&gt; Bovine sp.

&lt;400&gt; 46

Val	Leu	Asn	Ile	Ser	Leu	Trp
1				5		

&lt;210&gt; 47

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Bovine sp.

&lt;400&gt; 47

Thr	Leu	Met	Glu	Leu	Leu	Asn	Gln	Met	Asp	Gly	Phe	Asp	Thr	Leu	His
1				5					10					15	

Arg

&lt;210&gt; 48

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Bovine sp.

&lt;220&gt;

&lt;223&gt; all "Xaa" amino acids are unidentified

&lt;400&gt; 48

Ala	Val	Ser	Asp	Phe	Val	Val	Ser	Glu	Tyr	Xaa	Met	Xaa	Ala
1				5					10				

&lt;210&gt; 49

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Bovine sp.

<220>

<223> all "Xaa" amino acids are unidentified

<400> 49

Glu Val Asp Pro Leu Val Tyr Asn Xaa

1

5

<210> 50

<211> 11

<212> PRT

<213> Bovine sp.

<400> 50

His Gly Glu Ile Asp Tyr Glu Ala Ile Val Lys

1

5

10

<210> 51

<211> 25

<212> PRT

<213> Bovine sp.

<220>

<223> all "Xaa" amino acids are unidentified

<400> 51

Leu Ser Xaa Gly Phe Asn Gly Ala Asp Leu Arg Asn Val Xaa Thr Glu

1

5

10

15

Ala Gly Met Phe Ala Ile Xaa Ala Asp

20

25

<210> 52

<211> 21

<212> PRT

<213> Bovine sp.

<220>

<223> all "Xaa" amino acids are unidentified

<400> 52

Met Ile Met Ala Thr Asn Arg Pro Asp Thr Leu Asp Pro Ala Leu Leu

1

5

10

15

Arg Pro Gly Xaa Leu

20

<210> 53

<211> 16

<212> PRT

<213> Bovine sp.

<400> 53

Ile His Ile Asp Leu Pro Asn Glu Gln Ala Arg Leu Asp Ile Leu Lys

1

5

10

15

<210> 54  
 <211> 11  
 <212> PRT  
 <213> Bovine sp.

<400> 54  
 Ala Thr Asn Gly Pro Arg Tyr Val Val Val Gly  
           1                          5                          10

<210> 55  
 <211> 7  
 <212> PRT  
 <213> Bovine sp.

<400> 55  
 Glu Ile Asp Gly Arg Leu Lys  
           1                          5

<210> 56  
 <211> 14  
 <212> PRT  
 <213> Bovine sp.

<400> 56  
 Ala Leu Gln Ser Val Gly Gln Ile Val Gly Glu Val Leu Lys  
           1                          5                          10

<210> 57  
 <211> 8  
 <212> PRT  
 <213> Bovine sp.

<400> 57  
 Ile Leu Ala Gly Pro Ile Thr Lys  
           1                          5

<210> 58  
 <211> 16  
 <212> PRT  
 <213> Bovine sp.

<220>  
 <223> all "Xaa" amino acids are unidentified

<400> 58  
 Xaa Xaa Val Ile Glu Leu Pro Leu Thr Asn Pro Glu Leu Phe Gln Gly  
           1                          5                          10                          15

<210> 59  
 <211> 9  
 <212> PRT

<213> Bovine sp.

<400> 59

Val Val Ser Ser Ser Leu Val Asp Lys  
1 5

<210> 60

<211> 7

<212> PRT

<213> Bovine sp.

<400> 60

Ala Leu Gln Asp Tyr Arg Lys  
1 5

<210> 61

<211> 7

<212> PRT

<213> Bovine sp.

<400> 61

Glu His Arg Glu Gln Leu Lys  
1 5

<210> 62

<211> 12

<212> PRT

<213> Bovine sp.

<400> 62

Lys Leu Glu Ser Lys Leu Asp Tyr Lys Pro Val Arg  
1 5 10

<210> 63

<211> 5

<212> PRT

<213> Bovine sp.

<400> 63

Leu Val Pro Thr Arg  
1 5

<210> 64

<211> 11

<212> PRT

<213> Bovine sp.

<400> 64

Ala Lys Glu Glu Glu Ile Glu Ala Gln Ile Lys  
1 5 10

<210> 65



<211> 10  
 <212> PRT  
 <213> Bovine sp.

<400> 65  
 Ala Asn Tyr Glu Val Leu Glu Ser Gln Lys  
     1                    5                    10

<210> 66  
 <211> 11  
 <212> PRT  
 <213> Bovine sp.

<400> 66  
 Val Glu Asp Ala Leu His Gln Leu His Ala Arg  
     1                    5                    10

<210> 67  
 <211> 8  
 <212> PRT  
 <213> Bovine sp.

<400> 67  
 Asp Val Asp Leu Tyr Gln Val Arg  
     1                    5

<210> 68  
 <211> 13  
 <212> PRT  
 <213> Bovine sp.

<400> 68  
 Gln Ser Gln Gly Leu Ser Pro Ala Gln Ala Phe Ala Lys  
     1                    5                    10

<210> 69  
 <211> 21  
 <212> PRT  
 <213> Bovine sp.

<400> 69  
 Ala Gly Ser Gln Ser Gly Gly Ser Pro Glu Ala Ser Gly Val Thr Val  
     1                    5                    10                    15  
 Ser Asp Val Gln Glu  
                     20

<210> 70  
 <211> 12  
 <212> PRT  
 <213> Bovine sp.

<220>

<223> all "Xaa" amino acids are unidentified

<400> 70

Gly Leu Leu Gly Xaa Asn Ile Ile Pro Leu Gln Arg  
 1 5 10

<210> 71

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer P1

<400> 71

ttgaagaatg atgcattagg aaccac

26

<210> 72

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer P2

<400> 72

cactcgagtg gctggatttc aatttctcca gtag

34

<210> 73

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer P3

<400> 73

gtcgagctag ccatctcctc ttcg

24

<210> 74

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer P4

<400> 74

catgggagac aggttccgag acc

23

<210> 75

<211> 9

<212> PRT

<213> Homo sapiens

<400> 75

Lys Gly Ile Pro Ser Phe Trp Leu Thr  
1 5

<210> 76

<211> 9

<212> PRT

<213> Saccharomyces sp.

<400> 76

Lys Gly Ile Pro Glu Phe Trp Leu Thr  
1 5

<210> 77

<211> 10

<212> PRT

<213> Homo sapiens

<400> 77

Asp Ser Phe Phe Asn Phe Phe Ala Pro Pro  
1 5 10

<210> 78

<211> 9

<212> PRT

<213> Saccharomyces sp.

<400> 78

Glu Ser Phe Phe Asn Phe Phe Ser Pro  
1 5

<210> 79

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus  
sequence

<220>

<223> all "Xaa" amino acids are unidentified

<400> 79

Glu Xaa Xaa Lys Glu Xaa Pro Glu Val Lys Xaa Glu Glu Lys  
1 5 10

<210> 80

<211> 5

<212> PRT

<213> HIV-1

<400> 80  
 Gly Arg Lys Lys Arg  
     1                    5

<210> 81  
 <211> 5  
 <212> PRT  
 <213> Homo sapiens

<400> 81  
 Lys Lys Lys Arg Lys  
     1                    5

<210> 82  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: A1 Primer

<400> 82  
 cctaaaaagt gtctaagtgc cagtt 25

<210> 83  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: A2 Primer

<400> 83  
 tcagtgaag ggaaggtaga acac 24

<210> 84  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: P1 Primer

<400> 84  
 taatgaattt catttttagga ggtcgg 26

<210> 85  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>

## &lt;223&gt; Description of Artificial Sequence: P2 Primer

&lt;400&gt; 85

atcttttggg aaagtaagat gagcc

25

&lt;210&gt; 86

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

## &lt;223&gt; Description of Artificial Sequence: C1 Primer

&lt;400&gt; 86

ggagactcac ctgctaattgt t

21

&lt;210&gt; 87

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

## &lt;223&gt; Description of Artificial Sequence: C4 Primer

&lt;400&gt; 87

ctcaaaagca gtctcttggc

20

&lt;210&gt; 88

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

## &lt;223&gt; Description of Artificial Sequence: Primer A

&lt;400&gt; 88

atgggagata cagtagtgga gc

22

&lt;210&gt; 89

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

## &lt;223&gt; Description of Artificial Sequence: Primer B

&lt;400&gt; 89

tcacatgatg ccgttggtga g

21

&lt;210&gt; 90

&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<400> 90  
 tggatcaagc caatacaaga ttcttgtgaa attacgactg atagtggcat g 51

<210> 91  
 <211> 117  
 <212> DNA  
 <213> Homo sapiens

<400> 91  
 tccatttggg aacaggagcg agtgcccctt tggatcaagc catacaagat tcttgtgatt 60  
 tcggctgata gtggcatgat tgaaccagtg gtcaatgctg tgtccatcca tcaggtg 117

<210> 92  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer C1

<400> 92  
 ctcagatcta tgggagatac agtagtggag c 31

<210> 93  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer C2

<400> 93  
 tcgagatctt cacatgatgc cgttggtgag 30

<210> 94  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: P1 Primer

<400> 94  
 gatttgtgct caataatcac tatctgaa 28

<210> 95  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: P2 Primer

<400> 95

ggttactagg atcacaaagt atgaattctg gaa

33